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          RAW SEQUENCE LISTING          DATE: 11/09/2000
          PATENT APPLICATION:  US/09/695,786   TIME: 11:59:10

          Input Set : A:\CR9981 US DIV Seq Listing.txt
          Output Set: N:\CRF3\11092000\I695786.raw

          SEQUENCE LISTING
      3 (1) GENERAL INFORMATION:
      5        (i) APPLICANT: RAMESCH V. NAIR
      6                       MARK S. PAYNE
      7                       DONALD E. TRIMBUR
      8                       FERNANDO VALLE
     10       (ii) TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF
     11                       GLYCEROL BY RECOMBINANT
     12                       ORGANISMS
     14      (iii) NUMBER OF SEQUENCES: 43
     16       (iv) CORRESPONDENCE ADDRESS:
     24            (A) ADDRESSEE: GENENCOR INTERNATIONAL, INC.
     25            (B) STREET: 4 CAMBRIDGE PLACE
     26                    1870 SOUTH WINTON ROAD
     27            (C) CITY: ROCHESTER
     28            (D) STATE: NEW YORK
     29            (E) COUNTRY: U.S.A.
     30            (F) ZIP: 14618
     32        (v) COMPUTER READABLE FORM:
     33            (A) MEDIUM TYPE: DISKETTE, 3.5 INCH
     34            (B) COMPUTER: IBM PC COMPATIBLE
     35            (C) OPERATING SYSTEM: MICROSOFT WINDOWS 95
     36            (D) SOFTWARE: MICROSOFT WORD VERSION 7.0A
     38       (vi) CURRENT APPLICATION DATA:
C--> 39            (A) APPLICATION NUMBER: US/09/695,786
C--> 40            (B) FILING DATE: 25-Oct-2000
     46            (C) CLASSIFICATION:
     43      (vii) PRIOR APPLICATION DATA:
     44            (A) APPLICATION NUMBER: 60/030602
     45            (B) FILING DATE: NOVEMBER 13, 1996
     48     (viii) ATTORNEY/AGENT INFORMATION:
     49            (A) NAME: FLOYD, LINDA AXAMETHY
     50            (B) REGISTRATION NUMBER: 33,692
     51            (C) REFERENCE/DOCKET NUMBER: CR-9981-B
     53       (ix) TELECOMMUNICATION INFORMATION:
     54            (A) TELEPHONE: 302-892-8112
     55            (B) TELEFAX: 302-773-0164
     58 (2) INFORMATION FOR SEQ ID NO: 1:
     60        (i) SEQUENCE CHARACTERISTICS:
     61            (A) LENGTH: 1380 base pairs
     62            (B) TYPE: nucleic acid
     63            (C) STRANDEDNESS: single
     64            (D) TOPOLOGY: linear
     66       (ii) MOLECULE TYPE: DNA (genomic)
C--> 68       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
     70 CTTTAATTTT CTTTTATCTT ACTCTCCTAC ATAAGACATC AAGAAACAAT TGTATATTGT      60
     72 ACACCCCCCC CCTCCACAAA CACAAATATT GATAATATAA AGATGTCTGC TGCTGCTGAT     120
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          Input Set : A:\CR9981 US DIV Seq Listing.txt
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 74 AGATTAAACT TAACTTCCGG CCACTTGAAT GCTGGTAGAA AGAGAAGTTC CTCTTCTGTT  180
 76 TCTTTGAAGG CTGCCGAAAA GCCTTTCAAG GTTACTGTGA TTGGATCTGG TAACTGGGGT  240
 78 ACTACTATTG CCAAGGTGGT TGCCGAAAAT TGTAAGGGAT ACCCAGAAGT TTTCGCTCCA  300
 80 ATAGTACAAA TGTGGGTGTT CGAAGAAGAG ATCAATGGTG AAAAATTGAC TGAAATCATA  360
 82 AATACTAGAC ATCAAAACGT GAAATACTTG CCTGGCATCA CTCTACCCGA CAATTTGGTT  420
 84 GCTAATCCAG ACTTGATTGA TTCAGTCAAG GATGTCGACA TCATCGTTTT CAACATTCCA  480
 86 CATCAATTTT TGCCCCGTAT CTGTAGCCAA TTGAAAGGTC ATGTTGATTC ACACGTCAGA  540
 88 GCTATCTCCT GTCTAAAGGG TTTTGAAGTT GGTGCTAAAG GTGTCCAATT GCTATCCTCT  600
 90 TACATCACTG AGGAACTAGG TATTCAATGC GGTGCTCTAT CTGGTGCTAA CATTGCCACC  660
 92 GAAGTCGCTC AAGAACACTG GTCTGAAACA ACAGTTGCTT ACCACATTCC AAAGGATTTC  720
 94 AGAGGCGAGG GCAAGGACGT CGACCATAAG GTTCTAAAGG CCTTGTTCCA CAGACCTTAC  780
 96 TTCCACGTTA GTGTCATCGA AGATGTTGCT GGTATCTCCA TCTGTGGTGC TTTGAAGAAC  840
 98 GTTGTTGCCT TAGGTTGTGG TTTCGTCGAA GGTCTAGGCT GGGGTAACAA CGCTTCTGCT  900
100 GCCATCCAAA GAGTCGGTTT GGGTGAGATC ATCAGATTCG GTCAAATGTT TTTCCCAGAA  960
102 TCTAGAGAAG AAACATACTA CCAAGAGTCT GCTGGTGTTG CTGATTTGAT CACCACCTGC 1020
104 GCTGGTGGTA GAAACGTCAA GGTTGCTAGG CTAATGGCTA CTTCTGGTAA GGACGCCTGG 1080
106 GAATGTGAAA AGGAGTTGTT GAATGGCCAA TCCGCTCAAG GTTTAATTAC CTGCAAAGAA 1140
108 GTTCACGAAT GGTTGGAAAC ATGTGGCTCT GTCGAAGACT TCCCATTATT TGAAGCCGTA 1200
110 TACCAAATCG TTTACAACAA CTACCCAATG AAGAACCTGC CGGACATGAT TGAAGAATTA 1260
112 GATCTACATG AAGATTAGAT TTATTGGAGA AAGATAACAT ATCATACTTC CCCCACTTTT 1320
114 TTCGAGGCTC TTCTATATCA TATTCATAAA TTAGCATTAT GTCATTTCTC ATAACTACTT 1380
116 (2) INFORMATION FOR SEQ ID NO: 2:
118      (i) SEQUENCE CHARACTERISTICS:
119          (A) LENGTH: 2946 base pairs
120          (B) TYPE: nucleic acid
121          (C) STRANDEDNESS: single
122          (D) TOPOLOGY: linear
124      (ii) MOLECULE TYPE: DNA (genomic)
C-->126      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
128 GAATTCGAGC CTGAAGTGCT GATTACCTTC AGGTAGACTT CATCTTGACC CATCAACCCC   60
130 AGCGTCAATC CTGCAAATAC ACCACCCAGC AGCACTAGGA TGATAGAGAT AATATAGTAC  120
132 GTGGTAACGC TTGCCTCATC ACCTACGCTA TGGCCGGAAT CGGCAACATC CCTAGAATTG  180
134 AGTACGTGTG ATCCGGATAA CAACGGCAGT GAATATATCT TCGGTATCGT AAAGATGTGA  240
136 TATAAGACGA TGTATACCCA ATGAGGAGCG CCTGATCGTG ACCTAGACCT TAGTGGCAAA  300
138 AACGACATAT CTATTATAGT GGGGAGAGTT TCGTGCAAAT AACAGACGCA GCAGCAAGTA  360
140 ACTGTGACGA TATCAACTCT TTTTTTATTA TGTAATAAGC AAACAAGCAC GAATGGGGAA  420
142 AGCCTATGTG CAATCACCAA GGTCGTCCCT TTTTTCCCAT TTGCTAATTT AGAATTTAAA  480
144 GAAACCAAAA GAATGAAGAA AGAAAACAAA TACTAGCCCT AACCCTGACT TCGTTTCTAT  540
146 GATAATACCC TGCTTTAATG AACGGTATGC CCTAGGGTAT ATCTCACTCT GTACGTTACA  600
148 AACTCCGGTT ATTTTATCGG AACATCCGAG CACCCGCGCG TTCCTCAACC CAGGCACCGC  660
150 CCCAGGTAAC CGTGCGCGAT GAGCTAATCC TGAGCCATCA CCCACCCCAC CCGTTGATGA  720
152 CAGCAATTCG GGAGGGCGAA AATAAAACTG GAGCAAGGAA TTACCATCAC CGTCACCATC  780
154 ACCATCATAT CGCCTTAGCC TCTAGCCATA GCCATCATGC AAGCGTGTAT CTTCTAAGAT  840
156 TCAGTCATCA TCATTACCGA GTTTGTTTTC CTTCACATGA TGAAGAAGGT TTGAGTATGC  900
158 TCGAAACAAT AAGACGACGA TGGCTCTGCC ATTGGTTATA TTACGCTTTT GCGGCGAGGT  960
160 GCCGATGGGT TGCTGAGGGG AAGAGTGTTT AGCTTACGGA CCTATTGCCA TTGTTATTCC 1020
162 GATTAATCTA TTGTTCAGCA GCTCTTCTCT ACCCTGTCAT TCTAGTATTT TTTTTTTTTT 1080
164 TTTTTGGTTT TACTTTTTTT TCTTCTTGCC TTTTTTTCTT GTTACTTTTT TTCTAGTTTT 1140
166 TTTTCCTTCC ACTAAGCTTT TTCCTTGATT TATCCTTGGG TTCTTCTTTC TACTCCTTTA 1200
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RAW SEQUENCE LISTING   DATE: 11/09/2000
PATENT APPLICATION: US/09/695,786   TIME: 11:59:11

Input Set : A:\CR9981 US DIV Seq Listing.txt
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168 GATTTTTTTT TTATATATTA ATTTTTAAGT TTATGTATTT TGGTAGATTC AATTCTCTTT 1260
170 CCCTTTCCTT TTCCTTCGCT CCCCTTCCTT ATCAATGCTT GCTGTCAGAA GATTAACAAG 1320
172 ATACACATTC CTTAAGCGAA CGCATCCGGT GTTATATACT CGTCGTGCAT ATAAAATTTT 1380
174 GCCTTCAAGA TCTACTTTCC TAAGAAGATC ATTATTACAA ACACAACTGC ACTCAAAGAT 1440
176 GACTGCTCAT ACTAATATCA AACAGCACAA ACACTGTCAT GAGGACCATC CTATCAGAAG 1500
178 ATCGGACTCT GCCGTGTCAA TTGTACATTT GAAACGTGCG CCCTTCAAGG TTACAGTCAT 1560
180 TGGTTCTGGT AACTGGGGGA CCACCATCGC CAAAGTCATT GCGGAAAACA CAGAATTGCA 1620
182 TTCCCATATC TTCGAGCCAG AGGTGAGAAT GTGGGTTTTT GATGAAAAGA TCGGCGACGA 1680
184 AAATCTGACG GATATCATAA ATACAAGACA CCAGAACGTT AAATATCTAC CCAATATTGA 1740
186 CCTGCCCCAT AATCTAGTGG CCGATCCTGA TCTTTTACAC TCCATCAAGG GTGCTGACAT 1800
188 CCTTGTTTTC AACATCCCTC ATCAATTTTT ACCAAACATA GTCAAACAAT TGCAAGGCCA 1860
190 CGTGGCCCCT CATGTAAGGG CCATCTCGTG TCTAAAAGGG TTCGAGTTGG GCTCCAAGGG 1920
192 TGTGCAATTG CTATCCTCCT ATGTTACTGA TGAGTTAGGA ATCCAATGTG GCGCACTATC 1980
194 TGGTGCAAAC TTGGCACCGG AAGTGGCCAA GGAGCATTGG TCCGAAACCA CCGTGGCTTA 2040
196 CCAACTACCA AAGGATTATC AAGGTGATGG CAAGGATGTA GATCATAAGA TTTTGAAATT 2100
198 GCTGTTCCAC AGACCTTACT TCCACGTCAA TGTCATCGAT GATGTTGCTG GTATATCCAT 2160
200 TGCCGGTGCC TTGAAGAACG TCGTGGCACT TGCATGTGGT TTCGTAGAAG GTATGGGATG 2220
202 GGGTAACAAT GCCTCCGCAG CCATTCAAAG GCTGGGTTTA GGTGAAATTA TCAAGTTCGG 2280
204 TAGAATGTTT TTCCCAGAAT CCAAAGTCGA GACCTACTAT CAAGAATCCG CTGGTGTTGC 2340
206 AGATCTGATC ACCACCTGCT CAGGCGGTAG AAACGTCAAG GTTGCCACAT ACATGGCCAA 2400
208 GACCGGTAAG TCAGCCTTGG AAGCAGAAAA GGAATTGCTT AACGGTCAAT CCGCCCAAGG 2460
210 GATAATCACA TGCAGAGAAG TTCACGAGTG GCTACAAACA TGTGAGTTGA CCCAAGAATT 2520
212 CCCAATTATT CGAGGCAGTC TACCAGATAG TCTACAACAA CGTCCGCATG GAAGACCTAC 2580
214 CGGAGATGAT TGAAGAGCTA GACATCGATG ACGAATAGAC ACTCTCCCCC CCCCTCCCCC 2640
216 TCTGATCTTT CCTGTTGCCT CTTTTTCCCC CAACCAATTT ATCATTATAC ACAAGTTCTA 2700
218 CAACTACTAC TAGTAACATT ACTACAGTTA TTATAATTTT CTATTCTCTT TTTCTTTAAG 2760
220 AATCTATCAT TAACGTTAAT TTCTATATAT ACATAACTAC CATTATACAC GCTATTATCG 2820
222 TTTACATATC ACATCACCGT TAATGAAAGA TACGACACCC TGTACACTAA CACAATTAAA 2880
224 TAATCGCCAT AACCTTTTCT GTTATCTATA GCCCTTAAAG CTGTTTCTTC GAGCTTTTCA 2940
226 CTGCAG                                                         2946
228 (2) INFORMATION FOR SEQ ID NO: 3:
230     (i) SEQUENCE CHARACTERISTICS:
231         (A) LENGTH: 3178 base pairs
232         (B) TYPE: nucleic acid
233         (C) STRANDEDNESS: single
234         (D) TOPOLOGY: linear
236     (ii) MOLECULE TYPE: DNA (genomic)
238     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
240 CTGCAGAACT TCGTCTGCTC TGTGCCCATC CTCGCGGTTA GAAAGAAGCT GAATTGTTTC  60
242 ATGCGCAAGG GCATCAGCGA GTGACCAATA ATCACTGCAC TAATTCCTTT TTAGCAACAC 120
244 ATACTTATAT ACAGCACCAG ACCTTATGTC TTTTCTCTGC TCCGATACGT TATCCCACCC 180
246 AACTTTTATT TCAGTTTTGG CAGGGGAAAT TTCACAACCC CGCACGCTAA AAATCGTATT 240
248 TAAACTTAAA AGAGAACAGC CACAAATAGG GAACTTTGGT CTAAACGAAG GACTCTCCCT 300
250 CCCTTATCTT GACCGTGCTA TTGCCATCAC TGCTACAAGA CTAAATACGT ACTAATATAT 360
252 GTTTTCGGTA ACGAGAAGAA GAGCTGCCGG TGCAGCTGCT GCCATGGCCA CAGCCACGGG 420
254 GACGCTGTAC TGGATGACTA GCCAAGGTGA TAGGCCGTTA GTGCACAATG ACCCGAGCTA 480
256 CATGGTGCAA TTCCCCACCG CCGCTCCACC GGCAGGTCTC TAGACGAGAC CTGCTGGACC 540
258 GTCTGGACAA GACGCATCAA TTCGACGTGT TGATCATCGG TGGCGGGGCC ACGGGGACAG 600
260 GATGTGCCCT AGATGCTGCG ACCAGGGGAC TCAATGTGGC CCTTGTTGAA AAGGGGGATT 660
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C--> 238

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262 TTGCCTCGGG AACGTCGTCC AAATCTACCA AGATGATTCA CGGTGGGGTG CGGTACTTAG  720
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266 AGCGTAAACA TCTTATCAAC ACTGCCCCTC ACCTGTGCAC GGTGCTACCA ATTCTGATCC  840
268 CCATCTACAG CACCTGGCAG GTCCCGTACA TCTATATGGG CTGTAAATTC TACGATTTCT  900
270 TTGGCGGTTC CCAAAACTTG AAAAAATCAT ACCTACTGTC CAAATCCGCC ACCGTGGAGA  960
272 AGGCTCCCAT GCTTACCACA GACAATTTAA AGGCCTCGCT TGTGTACCAT GATGGGTCCT  1020
274 TTAACGACTC GCGTTTGAAC GCCACTTTAG CCATCACGGG TGTGGAGAAC GGCGCTACCG  1080
276 TCTTGATCTA TGTCGAGGTA CAAAAATTGA TCAAAGACCC AACTTCTGGT AAGGTTATCG  1140
278 GTGCCGAGGC CCGGGACGTT GAGACTAATG AGCTTGTCAG AATCAACGCT AAATGTGTGG  1200
280 TCAATGCCAC GGGCCCATAC AGTGACGCCA TTTTGCAAAT GGACCGCAAC CCATCCGGTC  1260
282 TGCCGGACTC CCCGCTAAAC GACAACTCCA AGATCAAGTC GACTTTCAAT CAAATCTCCG  1320
284 TCATGGACCC GAAAATGGTC ATCCCATCTA TTGGCGTTCA CATCGTATTG CCCTCTTTTT  1380
286 ACTCCCCGAA GGATATGGGT TTGTTGGACG TCAGAACCTC TGATGGCAGA GTGATGTTCT  1440
288 TTTTACCTTG GCAGGGCAAA GTCCTTGCCG GCACCACAGA CATCCCACTA AAGCAAGTCC  1500
290 CAGAAAACCC TATGCCTACA GAGGCTGATA TTCAAGATAT CTTGAAAGAA CTACAGCACT  1560
292 ATATCGAATT CCCCGTGAAA AGAGAAGACG TGCTAAGTGC ATGGGCTGGT GTCAGACCTT  1620
294 TGGTCAGAGA TCCACGTACA ATCCCCGCAG ACGGGAAGAA GGGCTCTGCC ACTCAGGGCG  1680
296 TGGTAAGATC CCACTTCTTG TTCACTTCGG ATAATGGCCT AATTACTATT GCAGGTGGTA  1740
298 AATGGACTAC TTACAGACAA ATGGCTGAGG AAACAGTCGA CAAAGTTGTC GAAGTTGGCG  1800
300 GATTCCACAA CCTGAAACCT TGTCACACAA GAGATATTAA GCTTGCTGGT GCAGAAGAAT  1860
302 GGACGCAAAA CTATGTGGCT TTATTGGCTC AAAACTACCA TTTATCATCA AAAATGTCCA  1920
304 ACTACTTGGT TCAAAACTAC GGAACCCGTT CCTCTATCAT TTGCGAATTT TTCAAAGAAT  1980
306 CCATGGAAAA TAAACTGCCT TTGTCCTTAG CCGACAAGGA AAATAACGTA ATCTACTCTA  2040
308 GCGAGGAGAA CAACTTGGTC AATTTTGATA CTTTCAGATA TCCATTCACA ATCGGTGAGT  2100
310 TAAAGTATTC CATGCAGTAC GAATATTGTA GAACTCCCTT GGACTTCCTT TTAAGAAGAA  2160
312 CAAGATTCGC CTTCTTGGAC GCCAAGGAAG CTTTGAATGC CGTGCATGCC ACCGTCAAAG  2220
314 TTATGGGTCA TGAGTTCAAT TGGTCGGAGA AAAAGAGGCA GTGGGAACTT GAAAAAACTG  2280
316 TGAACTTCAT CCAAGGACGT TTCGGTGTCT AAATCGATCA TGATAGTTAA GGGTGACAAA  2340
318 GATAACATTC ACAAGAGTAA TAATAATGGT AATGATGATA ATAATAATAA TGATAGTAAT  2400
320 AACAATAATA ATAATGGTGG TAATGGCAAT GAAATCGCTA TTATTACCTA TTTTTCCTTAA  2460
322 TGGAAGAGTT AAAGTAAACT AAAAAAAACTA CAAAAATATA TGAAGAAAAA AAAAAAAAGA  2520
324 GGTAATAGAC TCTACTACTA CAATTGATCT TCAAATTATG ACCTTCCTAG TGTTTATATT  2580
326 CTATTTCCAA TACATAATAT AATCTATATA ATCATTGCTG GTAGACTTCC GTTTTAATAT  2640
328 CGTTTTAATT ATCCCCTTTA TCTCTAGTCT AGTTTTATCA TAAAATATAG AAACACTAAA  2700
330 TAATATTCTT CAAACGGTCC TGGTGCATAC GCAATACATA TTTATGGTGC AAAAAAAAAA  2760
332 ATGGAAAATT TTGCTAGTCA TAAACCCTTT CATAAAACAA TACGTAGACA TCGCTACTTG  2820
334 AAATTTTCAA GTTTTTATCA GATCCATGTT TCCTATCTGC CTTGACAACC TCATCGTCGA  2880
336 AATAGTACCA TTTAGAACGC CCAATATTCA CATTGTGTTC AAGGTCTTTA TTCACCAGTG  2940
338 ACGTGTAATG GCCATGATTA ATGTGCCTGT ATGGTTAACC ACTCCAAATA GCTTATATTT  3000
340 CATAGTGTCA TTGTTTTTCA ATATAATGTT TAGTATCAAT GGATATGTTA CGACGGTGTT  3060
342 ATTTTTCTTG GTCAAATCGT AATAAAATCT CGATAAATGG ATGACTAAGA TTTTTGGTAA  3120
344 AGTTACAAAA TTTATCGTTT TCACTGTTGT CAATTTTTTG TTCTTGTAAT CACTCGAG    3178
346 (2) INFORMATION FOR SEQ ID NO: 4:
348      (i) SEQUENCE CHARACTERISTICS:
349          (A) LENGTH: 816 base pairs
350          (B) TYPE: nucleic acid
351          (C) STRANDEDNESS: single
352          (D) TOPOLOGY: linear
354      (ii) MOLECULE TYPE: DNA (genomic)
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RAW SEQUENCE LISTING                    DATE: 11/09/2000
PATENT APPLICATION:  US/09/695,786      TIME: 11:59:11

Input Set : A:\CR9981 US DIV Seq Listing.txt
Output Set: N:\CRF3\11092000\I695786.raw
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     360 GCAATGCCTT TGACCACAAA ACCTTTATCT TTGAAAATCA ACGCCGCTCT ATTCGATGTT   120
     362 GACGGTACCA TCATCATCTC TCAACCAGCC ATTGCTGCTT TCTGGACAGA TTTCGGTAAA   180
     364 GACAAGCCTT ACTTCGATGC CGAACACGTT ATTCACATCT CTCACGGTTG GAGAACTTAC   240
     366 GATGCCATTG CCAAGTTCGC TCCAGACTTT GCTGATGAAG AATACGTTAA CAAGCTAGAA   300
     368 GGTGAAATCC CAGAAAAGTA CGGTGAACAC TCCATCGAAG TTCCAGGTGC TGTCAAGTTG   360
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     372 GACATGGCCA AGAAATGGTT CGACATTTTG AAGATCAAGA GACCAGAATA CTTCATCACC   480
     374 GCCAATGATG TCAAGCAAGG TAAGCCTCAC CCAGAACCAT ACTTAAAGGG TAGAAACGGT   540
     376 TTGGGTTTCC CAATTAATGA ACAAGACCCA TCCAAATCTA AGGTTGTTGT CTTTGAAGAC   600
     378 GCACCAGCTG GTATTGCTGC TGGTAAGGCT GCTGGCTGTA AAATCGTTGG TATTGCTACC   660
     380 ACTTTCGATT TGGACTTCTT GAAGGAAAAG GGTTGTGACA TCATTGTCAA GAACCACGAA   720
     382 TCTATCAGAG TCGGTGAATA CAACGCTGAA ACCGATGAAG TCGAATTGAT CTTTGATGAC   780
     384 TACTTATACG CTAAGGATGA CTTGTTGAAA TGGTAA                             816
     386 (2) INFORMATION FOR SEQ ID NO: 5:
     388      (i) SEQUENCE CHARACTERISTICS:
     389           (A) LENGTH: 753 base pairs
     390           (B) TYPE: nucleic acid
     391           (C) STRANDEDNESS: single
     392           (D) TOPOLOGY: linear
     394      (ii) MOLECULE TYPE: DNA (genomic)
C--> 396  .   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
     398 ATGGGATTGA CTACTAAACC TCTATCTTTG AAAGTTAACG CCGCTTTGTT CGACGTCGAC    60
     400 GGTACCATTA TCATCTCTCA ACCAGCCATT GCTGCATTCT GGAGGGATTT CGGTAAGGAC   120
     402 AAACCTTATT TCGATGCTGA ACACGTTATC CAAGTCTCGC ATGGTTGGAG AACGTTTGAT   180
     404 GCCATTGCTA AGTTCGCTCC AGACTTTGCC AATGAAGAGT ATGTTAACAA ATTAGAAGCT   240
     406 GAAATTCCGG TCAAGTACGG TGAAAAATCC ATTGAAGTCC CAGGTGCAGT TAAGCTGTGC   300
     408 AACGCTTTGA ACGCTCTACC AAAAGAGAAA TGGGCTGTGG CAACTTCCGG TACCCGTGAT   360
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     416 CCAGCAGGTA TTGCCGCCGG AAAAGCCGCC GGTTGTAAGA TCATTGGTAT TGCCACTACT   600
     418 TTCGACTTGG ACTTCCTAAA GGAAAAAGGC TGTGACATCA TTGTCAAAAA CCACGAATCC   660
     420 ATCAGAGTTG GCGGCTACAA TGCCGAAACA GACGAAGTTG AATTCATTTT TGACGACTAC   720
     422 TTATATGCTA AGGACGATCT GTTGAAATGC TAA                                753
     424 (2) INFORMATION FOR SEQ ID NO: 6:
     426      (i) SEQUENCE CHARACTERISTICS:
     427           (A) LENGTH: 2520 base pairs
     428           (B) TYPE: nucleic acid
     429           (C) STRANDEDNESS: single
     430           (D) TOPOLOGY: linear
     432      (ii) MOLECULE TYPE: DNA (genomic)
C--> 434    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
     436 TGTATTGGCC ACGATAACCA CCCTTTGTAT ACTGTTTTTG TTTTTCACAT GGTAAATAAC    60
     438 GACTTTTATT AAACAACGTA TGTAAAAACA TAACAAGAAT CTACCCATAC AGGCCATTTC   120
     440 GTAATTCTTC TCTTCTAATT GGAGTAAAAC CATCAATTAA AGGGTGTGGA GTAGCATAGT   180
     442 GAGGGGCTGA CTGCATTGAC AAAAAAATTG AAAAAAAAAA AGGAAAAGGA AAGGAAAAAA   240
     444 AGACAGCCAA GACTTTTAGA ACGGATAAGG TGTAATAAAA TGTGGGGGGA TGCCTGTTCT   300
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VERIFICATION SUMMARY   DATE: 11/09/2000
PATENT APPLICATION: US/09/695,786   TIME: 11:59:12

Input Set : A:\CR9981 US DIV Seq Listing.txt
Output Set: N:\CRF3\11092000\I695786.raw

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L:40 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:68 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:126 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:238 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
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L:1129 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1189 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1252 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1399 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
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L:1469 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1483 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1497 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
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